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Informal Communication

# TELECOPY COVER SHEET

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**Proposed Claim Amendment**

**(Discussion only, Do NOT enter into file)**

16. A method for detecting the presence of contamination in a second sample by an amplicon from a previous sample, said method comprising the steps of:

conducting a first nucleic acid amplification reaction in a first sample comprising a first target nucleic acid, using at least one primer comprising a first portion that hybridizes with at least a portion of said first target nucleic acid, the amplification of which is desired, and a second portion that does not hybridize with said first target nucleic acid;

conducting a second nucleic acid amplification reaction in a second sample comprising a second target nucleic acid, using at least one primer comprising said second portion of said first primer; and

detecting the presence of an amplicon in said second reaction as indication of contamination in said second sample by an amplicon from said first amplification reaction.

17. The method of claim 16, wherein said second portion is not complementary to any contiguous nucleic acid sequence of said first target prior to said first nucleic acid amplification reaction.

18. The method of claim 16, wherein said first target nucleic acid comprises DNA.

19. The method of claim 16, wherein said first target nucleic acid comprises RNA.

20. The method of claim 16, wherein at least one of said nucleic acid amplification reactions is PCR.

21. The method of claim 16, wherein at least one of said nucleic acid amplification reactions is quantitative PCR.

22. The method of claim 16, wherein at least one of said nucleic acid amplification reactions is reverse-transcriptase PCR.

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23. The method of claim 16, wherein said amplicon is detected by sequence-specific nucleic acid probe capture.

24. The method of claim 16, wherein said first sample is a biological sample.

25. The method of claim 16, wherein said second sample is a biological sample.

26. The method of claim 16, wherein said second target nucleic acid comprises DNA.

27. The method of claim 16, wherein said first target nucleic acid is different from said second target nucleic acid.

28. The method of claim 16, wherein said first target nucleic acid and said second target nucleic acid are substantially the same.

29. A method for detecting contamination in a second sample by an amplicon from a previous sample, said method comprising the steps of:

conducting a first nucleic acid amplification reaction in a first sample comprising a first target nucleic acid template, using at least one chimeric primer, said primer comprising a template-specific sequence and a 5' contamination detection sequence;

conducting a second nucleic acid amplification reaction in a second sample comprising a second target nucleic acid template, using at least one primer that comprises said contamination detection sequence; and

detecting the presence of an amplicon in said second amplification reaction as indication of contamination in said second sample by an amplicon from said first amplification reaction.

30. The method of claim 29, wherein said first nuclei acid amplification reaction uses two chimeric primers.

31. The method of claim 29, wherein said second nucleic acid amplification reaction further uses a primer that hybridizes with said contamination detection sequence.

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32. The method of claim 29, wherein said contamination detection sequence is not complementary to any contiguous nucleic acid sequence of said first template prior to said first nucleic acid amplification reaction.

33. The method of claim 29, wherein the first target nucleic acid template comprises DNA.

34. The method of claim 29, wherein the second target nucleic acid template comprises DNA.

35. The method of claim 29, wherein at least one of said nucleic acid amplification reactions is PCR.

36. The method of claim 29, wherein at least one of said nucleic acid amplification reactions is quantitative PCR.

37. The method of claim 29, wherein at least one of said nucleic acid amplification reactions is reverse-transcriptase PCR.

38. The method of claim 29, wherein said first target nucleic acid template is different from said second target nucleic acid template.

39. The method of claim 29, wherein said first target nucleic acid template and said second target nucleic acid template are substantially the same.

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